

SEQUENCE LISTING

<110> Commissariat à l'Etude Atomique (CEA)
Centre National de la Recherche Scientifique (CNRS)

<120> A method for performing restrained dynamics docking of one or
multiple substrates on multi-specific enzymes

<130> D20647

<150> US 60/421,569

<151> 2002-10-28

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 403

<212> PRT

<213> Fusarium oxysporum

<220>

<223> P450 Nor, crystal structure from

<400> 1

Met Ala Ser Gly Ala Pro Ser Phe Pro Phe Ser Arg Ala Ser Gly Pro
1 5 10 15

Glu Pro Pro Ala Glu Phe Ala Lys Leu Arg Ala Thr Asn Pro Val Ser
20 25 30

Gln Val Lys Leu Phe Asp Gly Ser Leu Ala Trp Leu Val Thr Lys His
35 40 45

Lys Asp Val Cys Phe Val Ala Thr Ser Glu Lys Leu Ser Lys Val Arg
50 55 60

Thr Arg Gln Gly Phe Pro Glu Leu Ser Ala Ser Gly Lys Gln Ala Ala
65 70 75 80

Lys Ala Lys Pro Thr Phe Val Asp Met Asp Pro Pro Glu His Met His
85 90 95

Gln Arg Ser Met Val Glu Pro Thr Phe Thr Pro Glu Ala Val Lys Asn
100 105 110

Leu Gln Pro Tyr Ile Gln Arg Thr Val Asp Asp Leu Leu Glu Gln Met
115 120 125

Lys Gln Lys Gly Cys Ala Asn Gly Pro Val Asp Leu Val Lys Glu Phe
130 135 140

Ala Leu Pro Val Pro Ser Tyr Ile Ile Tyr Thr Leu Leu Gly Val Pro
145 150 155 160

Phe Asn Asp Leu Glu Tyr Leu Thr Gln Gln Asn Ala Ile Arg Thr Asn
165 170 175

Gly Ser Ser Thr Ala Arg Glu Ala Ser Ala Ala Asn Gln Glu Leu Leu
 180 185 190
 Asp Tyr Leu Ala Ile Leu Val Glu Gln Arg Leu Val Glu Pro Lys Asp
 195 200 205
 Asp Ile Ile Ser Lys Leu Cys Thr Glu Gln Val Lys Pro Gly Asn Ile
 210 215 220
 Asp Lys Ser Asp Ala Val Gln Ile Ala Phe Leu Leu Leu Val Ala Gly
 225 230 235 240
 Asn Ala Thr Met Val Asn Met Ile Ala Leu Gly Val Ala Thr Leu Ala
 245 250 255
 Gln His Pro Asp Gln Leu Ala Gln Leu Lys Ala Asn Pro Ser Leu Ala
 260 265 270
 Pro Gln Phe Val Glu Glu Leu Cys Arg Tyr His Thr Ala Ser Ala Leu
 275 280 285
 Ala Ile Lys Arg Thr Ala Lys Glu Asp Val Met Ile Gly Asp Lys Leu
 290 295 300
 Val Arg Ala Asn Glu Gly Ile Ile Ala Ser Asn Gln Ser Ala Asn Arg
 305 310 315 320
 Asp Glu Glu Val Phe Glu Asn Pro Asp Glu Phe Asn Met Asn Arg Lys
 325 330 335
 Trp Pro Pro Gln Asp Pro Leu Gly Phe Gly Phe Gly Asp His Arg Cys
 340 345 350
 Ile Ala Glu His Leu Ala Lys Ala Glu Leu Thr Thr Val Phe Ser Thr
 355 360 365
 Leu Tyr Gln Lys Phe Pro Asp Leu Lys Val Ala Val Pro Leu Gly Lys
 370 375 380
 Ile Asn Tyr Thr Pro Leu Asn Arg Asp Val Gly Ile Val Asp Leu Pro
 385 390 395 400
 Val Ile Phe

<210> 2
 <211> 403
 <212> PRT
 <213> Saccharopolyspora erythraea

<220>
 <223> P450 EryF, crystal structure loxa

<400> 2

Ala Thr Val Pro Asp Leu Glu Ser Asp Ser Phe His Val Asp Trp Tyr
 1 5 10 15
 Ser Thr Tyr Ala Glu Leu Arg Glu Thr Ala Pro Val Thr Pro Val Arg
 20 25 30

Phe Leu Gly Gln Asp Ala Trp Leu Val Thr Gly Tyr Asp Glu Ala Lys
35 40 45

Ala Ala Leu Ser Asp Leu Arg Leu Ser Ser Asp Pro Lys Lys Lys Tyr
50 55 60

Pro Gly Val Glu Val Glu Phe Pro Ala Tyr Leu Gly Phe Pro Glu Asp
65 70 75 80

Val Arg Asn Tyr Phe Ala Thr Asn Met Gly Thr Ser Asp Pro Pro Thr
85 90 95

His Thr Arg Leu Arg Lys Leu Val Ser Gln Glu Phe Thr Val Arg Arg
100 105 110

Val Glu Ala Met Arg Pro Arg Val Glu Gln Ile Thr Ala Glu Leu Leu
115 120 125

Asp Glu Val Gly Asp Ser Gly Val Val Asp Ile Val Asp Arg Phe Ala
130 135 140

His Pro Leu Pro Ile Lys Val Ile Cys Glu Leu Leu Gly Val Asp Glu
145 150 155 160

Ala Ala Arg Gly Ala Phe Gly Arg Trp Ser Ser Glu Ile Leu Val Met
165 170 175

Asp Pro Glu Arg Ala Glu Gln Arg Gly Gln Ala Ala Arg Glu Val Val
180 185 190

Asn Phe Ile Leu Asp Leu Val Glu Arg Arg Arg Thr Glu Pro Gly Asp
195 200 205

Asp Leu Leu Ser Ala Leu Ile Ser Val Gln Asp Asp Asp Gly Arg
210 215 220

Leu Ser Ala Asp Glu Leu Thr Ser Ile Ala Leu Val Leu Leu Ala
225 230 235 240

Gly Phe Glu Ala Ser Val Ser Leu Ile Gly Ile Gly Thr Tyr Leu Leu
245 250 255

Leu Thr His Pro Asp Gln Leu Ala Leu Val Arg Ala Asp Pro Ser Ala
260 265 270

Leu Pro Asn Ala Val Glu Glu Ile Leu Arg Tyr Ile Ala Pro Pro Glu
275 280 285

Thr Thr Thr Arg Phe Ala Ala Glu Glu Val Glu Ile Gly Gly Val Ala
290 295 300

Ile Pro Gln Tyr Ser Thr Val Leu Val Ala Asn Gly Ala Ala Asn Arg
305 310 315 320

Asp Pro Ser Gln Phe Pro Asp Pro His Arg Phe Asp Val Thr Arg Asp
325 330 335

Thr Arg Gly His Leu Ser Phe Gly Gln Gly Ile His Phe Cys Met Gly
340 345 350

Arg Pro Leu Ala Lys Leu Glu Gly Glu Val Ala Leu Arg Ala Leu Phe

355	360	365
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Gly Arg Phe Pro Ala Leu Ser Leu Gly Ile Asp Ala Asp Asp Val Val	370	375
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Trp Arg Arg Ser Leu Leu Leu Arg Gly Ile Asp His Leu Pro Val Arg	385	390
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380	395	400
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Leu Asp Gly

<210> 3
 <211> 412
 <212> PRT
 <213> Pseudomonas sp.

<220>
 <223> P450 Terp, crystal structure 1cpt

<400> 3

Met Asp Ala Arg Ala Thr Ile Pro Glu His Ile Ala Arg Thr Val Ile	1	5
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10	15
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Leu Pro Gln Gly Tyr Ala Asp Asp Glu Val Ile Tyr Pro Ala Phe Lys	20	25
---	----	----

30

Trp Leu Arg Asp Glu Gln Pro Leu Ala Met Ala His Ile Glu Gly Tyr	35	40
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45

Asp Pro Met Trp Ile Ala Thr Lys His Ala Asp Val Met Gln Ile Gly	50	55
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60

Lys Gln Pro Gly Leu Phe Ser Asn Ala Glu Gly Ser Glu Ile Leu Tyr	65	70
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75	80
----	----

Asp Gln Asn Asn Glu Ala Phe Met Arg Ser Ile Ser Gly Gly Cys Pro	85	90
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95

His Val Ile Asp Ser Leu Thr Ser Met Asp Pro Pro Thr His Thr Ala	100	105
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110

Tyr Arg Gly Leu Thr Leu Asn Trp Phe Gln Pro Ala Ser Ile Arg Lys	115	120
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125

Leu Glu Glu Asn Ile Arg Arg Ile Ala Gln Ala Ser Val Gln Arg Leu	130	135
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140

Leu Asp Phe Asp Gly Glu Cys Asp Phe Met Thr Asp Cys Ala Leu Tyr	145	150
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155

160

Tyr Pro Leu His Val Val Met Thr Ala Leu Gly Val Pro Glu Asp Asp	165	170
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175

Glu Pro Leu Met Leu Lys Leu Thr Gln Asp Phe Phe Gly Val Glu Ala	180	185
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190

Ala Arg Arg Phe His Glu Thr Ile Ala Thr Phe Tyr Asp Tyr Phe Asn	195	200
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205

Gly Phe Thr Val Asp Arg Arg Ser Cys Pro Lys Asp Asp Val Met Ser

210	215	220	
Leu Leu Ala Asn Ser Lys Leu Asp Gly Asn Tyr Ile Asp Asp Lys Tyr			
225	230	235	240
Ile Asn Ala Tyr Tyr Val Ala Ile Ala Thr Ala Gly His Asp Thr Thr			
245	250	255	
Ser Ser Ser Ser Gly Gly Ala Ile Ile Gly Leu Ser Arg Asn Pro Glu			
260	265	270	
Gln Leu Ala Leu Ala Lys Ser Asp Pro Ala Leu Ile Pro Arg Leu Val			
275	280	285	
Asp Glu Ala Val Arg Trp Thr Ala Pro Val Lys Ser Phe Met Arg Thr			
290	295	300	
Ala Leu Ala Asp Thr Glu Val Arg Gly Gln Asn Ile Lys Arg Gly Asp			
305	310	315	320
Arg Ile Met Leu Ser Tyr Pro Ser Ala Asn Arg Asp Glu Glu Val Phe			
325	330	335	
Ser Asn Pro Asp Glu Phe Asp Ile Thr Arg Phe Pro Asn Arg His Leu			
340	345	350	
Gly Phe Gly Trp Gly Ala His Met Cys Leu Gly Gln His Leu Ala Lys			
355	360	365	
Leu Glu Met Lys Ile Phe Phe Glu Glu Leu Leu Pro Lys Leu Lys Ser			
370	375	380	
Val Glu Leu Ser Gly Pro Pro Arg Leu Val Ala Thr Asn Phe Val Gly			
385	390	395	400
Gly Pro Lys Asn Val Pro Ile Arg Phe Thr Lys Ala			
405	410		
<210> 4			
<211> 414			
<212> PRT			
<213> Pseudomonas putida			
<220>			
<223> P450 Cam, crystal structure 3cpp			
<400> 4			
Thr Thr Glu Thr Ile Gln Ser Asn Ala Asn Leu Ala Pro Leu Pro Pro			
1	5	10	15
His Val Pro Glu His Leu Val Phe Asp Phe Asp Met Tyr Asn Pro Ser			
20	25	30	
Asn Leu Ser Ala Gly Val Gln Glu Ala Trp Ala Val Leu Gln Glu Ser			
35	40	45	
Asn Val Pro Asp Leu Val Trp Thr Arg Cys Asn Gly Gly His Trp Ile			
50	55	60	
Ala Thr Arg Gly Gln Leu Ile Arg Glu Ala Tyr Glu Asp Tyr Arg His			

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65	70	75	80
Phe Ser Ser Glu Cys Pro Phe Ile Pro Arg Glu Ala Gly Glu Ala Tyr			
85	90	95	
Asp Phe Ile Pro Thr Ser Met Asp Pro Pro Glu Gln Arg Gln Phe Arg			
100	105	110	
Ala Leu Ala Asn Gln Val Val Gly Met Pro Val Val Asp Lys Leu Glu			
115	120	125	
Asn Arg Ile Gln Glu Leu Ala Cys Ser Leu Ile Glu Ser Leu Arg Pro			
130	135	140	
Gln Gly Gln Cys Asn Phe Thr Glu Asp Tyr Ala Glu Pro Phe Pro Ile			
145	150	155	160
Arg Ile Phe Met Leu Leu Ala Gly Leu Pro Glu Glu Asp Ile Pro His			
165	170	175	
Leu Lys Tyr Leu Thr Asp Gln Met Thr Arg Pro Asp Gly Ser Met Thr			
180	185	190	
Phe Ala Glu Ala Lys Glu Ala Leu Tyr Asp Tyr Leu Ile Pro Ile Ile			
195	200	205	
Glu Gln Arg Arg Gln Lys Pro Gly Thr Asp Ala Ile Ser Ile Val Ala			
210	215	220	
Asn Gly Gln Val Asn Gly Arg Pro Ile Thr Ser Asp Glu Ala Lys Arg			
225	230	235	240
Met Cys Gly Leu Leu Leu Val Gly Gly Leu Asp Thr Val Val Asn Phe			
245	250	255	
Leu Ser Phe Ser Met Glu Phe Leu Ala Lys Ser Pro Glu His Arg Gln			
260	265	270	
Glu Leu Ile Glu Arg Pro Glu Arg Ile Pro Ala Ala Cys Glu Glu Leu			
275	280	285	
Leu Arg Arg Phe Ser Leu Val Ala Asp Gly Arg Ile Leu Thr Ser Asp			
290	295	300	
Tyr Glu Phe His Gly Val Gln Leu Lys Lys Gly Asp Gln Ile Leu Leu			
305	310	315	320
Pro Gln Met Leu Ser Gly Leu Asp Glu Arg Glu Asn Ala Cys Pro Met			
325	330	335	
His Val Asp Phe Ser Arg Gln Lys Val Ser His Thr Thr Phe Gly His			
340	345	350	
Gly Ser His Leu Cys Leu Gly Gln His Leu Ala Arg Arg Glu Ile Ile			
355	360	365	
Val Thr Leu Lys Glu Trp Leu Thr Arg Ile Pro Asp Phe Ser Ile Ala			
370	375	380	
Pro Gly Ala Gln Ile Gln His Lys Ser Gly Ile Val Ser Gly Val Gln			
385	390	395	400

Ala Leu Pro Leu Val Trp Asp Pro Ala Thr Thr Lys Ala Val
405 410

<210> 5
<211> 471
<212> PRT
<213> *Bacillus megaterium*

<220>
<223> P450 BM3, crystal structure 2hpd

<400> 5

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn
1 5 10 15

Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile
20 25 30

Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val
35 40 45

Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu
50 55 60

Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp
65 70 75 80

Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp
85 90 95

Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met
100 105 110

Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln
115 120 125

Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp
130 135 140

Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr
145 150 155 160

Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser
165 170 175

Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn
180 185 190

Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp
195 200 205

Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys
210 215 220

Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly
225 230 235 240

Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr

245	250	255
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Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu		
260	265	270

Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln		
275	280	285

Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser		
290	295	300

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu		
305	310	315
		320

Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys		
325	330	335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu		
340	345	350

Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly		
355	360	365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala		
370	375	380

Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys		
385	390	395
		400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met		
405	410	415

Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp		
420	425	430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala		
435	440	445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu		
450	455	460

Gln Ser Ala Lys Lys Val Arg		
465	470	

<210> 6

<211> 473

<212> PRT

<213> Rabbit

<220>

<223> P450 2C5, crystal structure 1dt6

<400> 6

Met Ala Lys Lys Thr Ser Ser Lys Gly Lys Leu Pro Pro Gly Pro Thr		
1	5	10
		15

Pro Phe Pro Ile Ile Gly Asn Ile Leu Gln Ile Asp Ala Lys Asp Ile		
20	25	30

Ser Lys Ser Leu Thr Lys Phe Ser Glu Cys Tyr Gly Pro Val Phe Thr
35 40 45

Val Tyr Leu Gly Met Lys Pro Thr Val Val Leu His Gly Tyr Glu Ala
50 55 60

Val Lys Glu Ala Leu Val Asp Leu Gly Glu Glu Phe Ala Gly Arg Gly
65 70 75 80

Ser Val Pro Ile Leu Glu Lys Val Ser Lys Gly Leu Gly Ile Ala Phe
85 90 95

Ser Asn Ala Lys Thr Trp Lys Glu Met Arg Arg Phe Ser Leu Met Thr
100 105 110

Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg Ile Gln
115 120 125

Glu Glu Ala Arg Cys Leu Val Glu Glu Leu Arg Lys Thr Asn Ala Ser
130 135 140

Pro Cys Asp Pro Thr Phe Ile Leu Gly Cys Ala Pro Cys Asn Val Ile
145 150 155 160

Cys Ser Val Ile Phe His Asn Arg Phe Asp Tyr Lys Asp Glu Glu Phe
165 170 175

Leu Lys Leu Met Glu Ser Leu His Glu Asn Val Glu Leu Leu Gly Thr
180 185 190

Pro Trp Leu Gln Val Tyr Asn Asn Phe Pro Ala Leu Leu Asp Tyr Phe
195 200 205

Pro Gly Ile His Lys Thr Leu Leu Lys Asn Ala Asp Tyr Ile Lys Asn
210 215 220

Phe Ile Met Glu Lys Val Lys Glu His Gln Lys Leu Leu Asp Val Asn
225 230 235 240

Asn Pro Arg Asp Phe Ile Asp Cys Phe Leu Ile Lys Met Glu Gln Glu
245 250 255

Asn Asn Leu Glu Phe Thr Leu Glu Ser Leu Val Ile Ala Val Ser Asp
260 265 270

Leu Phe Gly Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu Arg Tyr Ser
275 280 285

Leu Leu Leu Leu Lys His Pro Glu Val Ala Ala Arg Val Gln Glu
290 295 300

Glu Ile Glu Arg Val Ile Gly Arg His Arg Ser Pro Cys Met Gln Asp
305 310 315 320

Arg Ser Arg Met Pro Tyr Thr Asp Ala Val Ile His Glu Ile Gln Arg
325 330 335

Phe Ile Asp Leu Leu Pro Thr Asn Leu Pro His Ala Val Thr Arg Asp
340 345 350

Val Arg Phe Arg Asn Tyr Phe Ile Pro Lys Gly Thr Asp Ile Ile Thr

355 360 365

Ser Leu Thr Ser Val Leu His Asp Glu Lys Ala Phe Pro Asn Pro Lys
370 375 380

Val Phe Asp Pro Gly His Phe Leu Asp Glu Ser Gly Asn Phe Lys Lys
385 390 395 400

Ser Asp Tyr Phe Met Pro Phe Ser Ala Gly Lys Arg Met Cys Val Gly
405 410 415

Glu Gly Leu Ala Arg Met Glu Leu Phe Leu Phe Leu Thr Ser Ile Leu
420 425 430

Gln Asn Phe Lys Leu Gln Ser Leu Val Glu Pro Lys Asp Leu Asp Ile
435 440 445

Thr Ala Val Val Asn Gly Phe Val Ser Val Pro Pro Ser Tyr Gln Leu
450 455 460

Cys Phe Ile Pro Ile His His His His
465 470

<210> 7

<211> 487

<212> PRT

<213> Rabbit

<220>

<223> P450 2C5

<400> 7

Met Asp Pro Val Val Val Leu Val Leu Gly Leu Cys Cys Leu Leu Leu
1 5 10 15

Leu Ser Ile Trp Lys Gln Asn Ser Gly Arg Gly Lys Leu Pro Pro Gly
20 25 30

Pro Thr Pro Phe Pro Ile Ile Gly Asn Ile Leu Gln Ile Asp Ala Lys
35 40 45

Asp Ile Ser Lys Ser Leu Thr Lys Phe Ser Glu Cys Tyr Gly Pro Val
50 55 60

Phe Thr Val Tyr Leu Gly Met Lys Pro Thr Val Val Leu His Gly Tyr
65 70 75 80

Glu Ala Val Lys Glu Ala Leu Val Asp Leu Gly Glu Glu Phe Ala Gly
85 90 95

Thr Gly Ser Val Pro Ile Leu Glu Lys Val Ser Lys Gly Leu Gly Ile
100 105 110

Ala Phe Ser Asn Ala Lys Thr Trp Lys Glu Met Arg Arg Phe Ser Leu
115 120 125

Met Thr Leu Arg Asn Phe Gly Met Gly Lys Arg Ser Ile Glu Asp Arg
130 135 140

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Ile Gln Glu Glu Ala Arg Cys Leu Val Glu Glu Leu Arg Lys Thr Asn
145 150 155 160

Ala Ser Pro Cys Asp Pro Thr Phe Ile Leu Gly Cys Ala Pro Cys Asn
165 170 175

Val Ile Cys Ser Val Ile Phe His Asn Arg Phe Asp Tyr Lys Asp Glu
180 185 190

Glu Phe Leu Lys Leu Met Glu Ser Leu Asn Glu Asn Val Arg Ile Leu
195 200 205

Ser Ser Pro Trp Leu Gln Val Tyr Asn Asn Phe Pro Ala Leu Leu Asp
210 215 220

Tyr Phe Pro Gly Ile His Lys Thr Leu Leu Lys Asn Ala Asp Tyr Ile
225 230 235 240

Lys Asn Phe Ile Met Glu Lys Val Lys Glu His Glu Lys Leu Leu Asp
245 250 255

Val Asn Asn Pro Arg Asp Phe Ile Asp Cys Phe Leu Ile Lys Met Glu
260 265 270

Gln Glu Asn Asn Leu Glu Phe Thr Leu Glu Ser Leu Val Ile Ala Val
275 280 285

Ser Asp Leu Phe Gly Ala Gly Thr Glu Thr Thr Ser Thr Thr Leu Arg
290 295 300

Tyr Ser Leu Leu Leu Leu Lys His Pro Glu Val Ala Ala Arg Val
305 310 315 320

Gln Glu Glu Ile Glu Arg Val Ile Gly Arg His Arg Ser Pro Cys Met
325 330 335

Gln Asp Arg Ser Arg Met Pro Tyr Thr Asp Ala Val Ile His Glu Ile
340 345 350

Gln Arg Phe Ile Asp Leu Leu Pro Thr Asn Leu Pro His Ala Val Thr
355 360 365

Arg Asp Val Arg Phe Arg Asn Tyr Phe Ile Pro Lys Gly Thr Asp Ile
370 375 380

Ile Thr Ser Leu Thr Ser Val Leu His Asp Glu Lys Ala Phe Pro Asn
385 390 395 400

Pro Lys Val Phe Asp Pro Gly His Phe Leu Asp Glu Ser Gly Asn Phe
405 410 415

Lys Lys Ser Asp Tyr Phe Met Pro Phe Ser Ala Gly Lys Arg Met Cys
420 425 430

Val Gly Glu Gly Leu Ala Arg Met Glu Leu Phe Leu Phe Leu Thr Ser
435 440 445

Ile Leu Gln Asn Phe Lys Leu Gln Ser Leu Val Glu Pro Lys Asp Leu
450 455 460

Asp Ile Thr Ala Val Val Asn Gly Phe Val Ser Val Pro Pro Ser Tyr

465 470 475 480

Gln Leu Cys Phe Ile Pro Ile
485

<210> 8
<211> 455
<212> PRT
<213> *Mycobacterium tuberculosis*

<220>
<223> CYP51, crystal structure 1e9x

<400> 8

Met Ser Ala Val Ala Leu Pro Arg Val Ser Gly Gly His Asp Glu His
1 5 10 15

Gly His Leu Glu Glu Phe Arg Thr Asp Pro Ile Gly Leu Met Gln Arg
20 25 30

Val Arg Asp Glu Cys Gly Asp Val Gly Thr Phe Gln Leu Ala Gly Lys
35 40 45

Gln Val Val Leu Leu Ser Gly Ser His Ala Asn Glu Phe Phe Arg
50 55 60

Ala Gly Asp Asp Asp Leu Asp Gln Ala Lys Ala Tyr Pro Phe Met Thr
65 70 75 80

Pro Ile Phe Gly Glu Gly Val Val Phe Asp Ala Ser Pro Glu Arg Arg
85 90 95

Lys Glu Met Leu His Asn Ala Ala Leu Arg Gly Glu Gln Met Lys Gly
100 105 110

His Ala Ala Thr Ile Glu Asp Gln Val Arg Arg Met Ile Ala Asp Trp
115 120 125

Gly Glu Ala Gly Glu Ile Asp Leu Leu Asp Phe Phe Ala Glu Leu Thr
130 135 140

Ile Tyr Thr Ser Ser Ala Cys Leu Ile Gly Lys Lys Phe Arg Asp Gln
145 150 155 160

Leu Asp Gly Arg Phe Ala Lys Leu Tyr His Glu Leu Glu Arg Gly Thr
165 170 175

Asp Pro Leu Ala Tyr Val Asp Pro Tyr Leu Pro Ile Glu Ser Phe Arg
180 185 190

Arg Arg Asp Glu Ala Arg Asn Gly Leu Val Ala Leu Val Ala Asp Ile
195 200 205

Met Asn Gly Arg Ile Ala Asn Pro Pro Thr Asp Lys Ser Asp Arg Asp
210 215 220

Met Leu Asp Val Leu Ile Ala Val Lys Ala Glu Thr Gly Thr Pro Arg
225 230 235 240

Phe Ser Ala Asp Glu Ile Thr Gly Met Phe Ile Ser Met Met Phe Ala
 245 250 255
 Gly His His Thr Ser Ser Gly Thr Ala Ser Trp Thr Leu Ile Glu Leu
 260 265 270
 Met Arg His Arg Asp Ala Tyr Ala Ala Val Ile Asp Glu Leu Asp Glu
 275 280 285
 Leu Tyr Gly Asp Gly Arg Ser Val Ser Phe His Ala Leu Arg Gln Ile
 290 295 300
 Pro Gln Leu Glu Asn Val Leu Lys Glu Thr Leu Arg Leu His Pro Pro
 305 310 315 320
 Leu Ile Ile Leu Met Arg Val Ala Lys Gly Glu Phe Glu Val Gln Gly
 325 330 335
 His Arg Ile His Glu Gly Asp Leu Val Ala Ala Ser Pro Ala Ile Ser
 340 345 350
 Asn Arg Ile Pro Glu Asp Phe Pro Asp Pro His Asp Phe Val Pro Ala
 355 360 365
 Arg Tyr Glu Gln Pro Arg Gln Glu Asp Leu Leu Asn Arg Trp Thr Trp
 370 375 380
 Ile Pro Phe Gly Ala Gly Arg His Arg Cys Val Gly Ala Ala Phe Ala
 385 390 395 400
 Ile Met Gln Ile Lys Ala Ile Phe Ser Val Leu Leu Arg Glu Tyr Glu
 405 410 415
 Phe Glu Met Ala Gln Pro Pro Glu Ser Tyr Arg Asn Asp His Ser Lys
 420 425 430
 Met Val Val Gln Leu Ala Gln Pro Ala Cys Val Arg Tyr Arg Arg Arg
 435 440 445
 Thr Gly Val His His His
 450 455

<210> 9
 <211> 504
 <212> PRT
 <213> Rat

<220>
 <223> CYP3A1

<400> 9

Met Asp Leu Leu Ser Ala Leu Thr Leu Glu Thr Trp Val Leu Leu Ala
 1 5 10 15
 Val Val Leu Val Leu Leu Tyr Gly Phe Gly Thr Arg Thr His Gly Leu
 20 25 30
 Phe Lys Lys Gln Gly Ile Pro Gly Pro Lys Pro Leu Pro Phe Phe Gly
 35 40 45

Thr Val Leu Asn Tyr Tyr Met Gly Leu Trp Lys Phe Asp Val Glu Cys
50 55 60

His Lys Lys Tyr Gly Lys Ile Trp Gly Leu Phe Asp Gly Gln Met Pro
65 70 75 80

Leu Phe Ala Ile Thr Asp Thr Glu Met Ile Lys Asn Val Leu Val Lys
85 90 95

Glu Cys Phe Ser Val Phe Thr Asn Arg Arg Asp Phe Gly Pro Val Gly
100 105 110

Ile Met Gly Lys Ala Val Ser Val Ala Lys Asp Glu Glu Trp Lys Arg
115 120 125

Tyr Arg Ala Leu Leu Ser Pro Thr Phe Thr Ser Gly Arg Leu Lys Glu
130 135 140

Met Phe Pro Ile Ile Glu Gln Tyr Gly Asp Ile Leu Val Lys Tyr Leu
145 150 155 160

Lys Gln Glu Ala Glu Thr Gly Lys Pro Val Thr Met Lys Lys Val Phe
165 170 175

Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn
180 185 190

Val Asp Ser Leu Asn Asn Pro Lys Asp Pro Phe Val Glu Lys Thr Lys
195 200 205

Lys Leu Leu Arg Phe Asp Phe Phe Asp Pro Leu Phe Leu Ser Val Val
210 215 220

Leu Phe Pro Phe Leu Thr Pro Ile Tyr Glu Met Leu Asn Ile Cys Met
225 230 235 240

Phe Pro Lys Asp Ser Ile Glu Phe Phe Lys Lys Phe Val Tyr Arg Met
245 250 255

Lys Glu Thr Arg Leu Asp Ser Val Gln Lys His Arg Val Asp Phe Leu
260 265 270

Gln Leu Met Met Asn Ala His Asn Asp Ser Lys Asp Lys Glu Ser His
275 280 285

Thr Ala Leu Ser Asp Met Glu Ile Thr Ala Gln Ser Ile Ile Phe Ile
290 295 300

Phe Ala Gly Tyr Glu Pro Thr Ser Ser Thr Leu Ser Phe Val Leu His
305 310 315 320

Ser Leu Ala Thr His Pro Asp Thr Gln Lys Lys Leu Gln Glu Glu Ile
325 330 335

Asp Arg Ala Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Met
340 345 350

Glu Met Glu Tyr Leu Asp Met Val Leu Asn Glu Thr Leu Arg Leu Tyr
355 360 365

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Pro Ile Gly Asn Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile
370 375 380

Asn Gly Val Phe Met Pro Lys Gly Ser Val Val Met Ile Pro Ser Tyr
385 390 395 400

Ala Leu His Arg Asp Pro Gln His Trp Pro Glu Pro Glu Glu Phe Arg
405 410 415

Pro Glu Arg Phe Ser Lys Glu Asn Lys Gly Ser Ile Asp Pro Tyr Val
420 425 430

Tyr Leu Pro Phe Gly Asn Gly Pro Arg Asn Cys Ile Gly Met Arg Phe
435 440 445

Ala Leu Met Asn Met Lys Leu Ala Leu Thr Lys Val Leu Gln Asn Phe
450 455 460

Ser Phe Gln Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Arg
465 470 475 480

Gln Gly Leu Leu Gln Pro Thr Lys Pro Ile Ile Leu Lys Val Val Pro
485 490 495

Arg Asp Glu Ile Ile Thr Gly Ser
500

<210> 10
<211> 503
<212> PRT
<213> Homo sapiens

<220>
<223> CYP3A3

<400> 10

Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala Val
1 5 10 15

Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu Phe
20 25 30

Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly Asn
35 40 45

Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys His
50 55 60

Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro Val
65 70 75 80

Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Leu Val Leu Val Lys Glu
85 90 95

Cys Tyr Ser Val Phe Thr Asn Arg Glu Pro Phe Gly Pro Val Gly Phe
100 105 110

Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg Leu

16/31

	115	120	125
Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met	130	135	140
Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu Arg	145	150	155
Arg Glu Arg Glu Thr Gly Lys Pro Val Thr Leu Lys Asp Val Phe Gly	165	170	175
Ala Tyr Ser Met Asp Val Ile Thr Ser Ser Ser Phe Gly Val Asn Val	180	185	190
Asp Ser Leu Asn Asn Pro Gln Asp Pro Leu Val Glu Asn Thr Lys Lys	195	200	205
Leu Leu Arg Phe Asp Phe Leu Asp Pro Phe Phe Leu Ser Ile Thr Val	210	215	220
Phe Pro Phe Leu Ile Pro Ile Leu Glu Val Leu Asn Ile Cys Val Phe	225	230	235
Pro Arg Glu Val Thr Asn Phe Leu Arg Lys Ala Val Lys Arg Met Lys	245	250	255
Glu Ser Arg Leu Glu Asp Thr Gln Lys His Arg Val Asp Phe Leu Gln	260	265	270
Leu Met Ile Asp Ser His Lys Asn Ser Lys Glu Thr Glu Ser His Lys	275	280	285
Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe	290	295	300
Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Met Tyr Glu	305	310	315
Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp	325	330	335
Ala Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln	340	345	350
Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro	355	360	365
Ile Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn	370	375	380
Gly Met Phe Ile Pro Lys Gly Trp Val Val Met Ile Pro Ser Tyr Ala	385	390	395
Leu His Arg Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Leu Pro	405	410	415
Glu Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr	420	425	430
Thr Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala	435	440	445

Leu Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe Ser
450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Leu Gly
465 470 475 480

Gly Leu Leu Gln Pro Glu Lys Pro Val Val Leu Lys Val Glu Ser Arg
485 490 495

Asp Gly Thr Val Ser Gly Ala
500

<210> 11
<211> 502
<212> PRT
<213> Homo sapiens

<220>
<223> CYP3A4

<400> 11

Ala Leu Ile Pro Asp Leu Ala Met Glu Thr Trp Leu Leu Leu Ala Val
1 5 10 15

Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Leu Phe
20 25 30

Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly Asn
35 40 45

Ile Leu Ser Tyr His Lys Gly Phe Cys Met Phe Asp Met Glu Cys His
50 55 60

Lys Lys Tyr Gly Lys Val Trp Gly Phe Tyr Asp Gly Gln Gln Pro Val
65 70 75 80

Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys Glu
85 90 95

Cys Tyr Ser Val Phe Thr Asn Arg Arg Pro Phe Gly Pro Val Gly Phe
100 105 110

Met Lys Ser Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg Leu
115 120 125

Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met
130 135 140

Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu Arg
145 150 155 160

Arg Glu Ala Glu Thr Gly Lys Pro Val Thr Leu Lys Asp Val Phe Gly
165 170 175

Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn Ile
180 185 190

Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Thr Lys Lys

195	200	205
Leu Leu Arg Phe Asp Phe Leu Asp Pro Phe Phe Leu Ser Ile Thr Val		
210	215	220
Phe Pro Phe Leu Ile Pro Ile Leu Glu Val Leu Asn Ile Cys Val Phe		
225	230	235
240		
Pro Arg Glu Val Thr Asn Phe Leu Arg Lys Ser Val Lys Arg Met Lys		
245	250	255
Glu Ser Arg Leu Glu Asp Thr Gln Lys His Arg Val Asp Phe Leu Gln		
260	265	270
Leu Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Glu Ser His Lys Ala		
275	280	285
Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe Ala		
290	295	300
Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Met Tyr Glu Leu		
305	310	315
320		
Ala Thr His Pro Val Asp Gln Gln Lys Leu Gln Glu Glu Ile Asp Ala		
325	330	335
Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln Met		
340	345	350
Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro Ile		
355	360	365
Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn Gly		
370	375	380
Met Phe Ile Pro Lys Gly Trp Val Val Met Ile Pro Ser Tyr Ala Leu		
385	390	395
400		
His Arg Asp Pro Lys Tyr Met Thr Glu Pro Glu Lys Phe Leu Pro Glu		
405	410	415
Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr Thr		
420	425	430
Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala Leu		
435	440	445
Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe Ser Phe		
450	455	460
Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Ser Leu Gly Gly		
465	470	475
480		
Leu Leu Gln Pro Glu Lys Pro Val Val Leu Lys Val Glu Ser Arg Asp		
485	490	495
Gly Thr Val Ser Gly Ala		
500		

<211> 502
<212> PRT
<213> Homo sapiens

<220>
<223> CYP3A5

<400> 12

Met Asp Leu Ile Pro Asn Leu Ala Val Glu Thr Trp Leu Leu Leu Ala
1 5 10 15

Val Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Arg Thr His Gly Leu
20 25 30

Phe Lys Arg Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Leu Leu Gly
35 40 45

Asn Val Leu Ser Tyr Arg Gln Gly Leu Trp Lys Phe Asp Thr Glu Cys
50 55 60

Tyr Lys Lys Tyr Gly Lys Met Trp Gly Thr Tyr Glu Gly Gln Leu Pro
65 70 75 80

Val Leu Ala Ile Thr Asp Pro Asp Val Ile Arg Thr Val Leu Val Lys
85 90 95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Ser Leu Gly Pro Val Gly
100 105 110

Phe Met Lys Ser Ala Ile Ser Leu Ala Glu Asp Glu Glu Trp Lys Arg
115 120 125

Ile Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
130 135 140

Met Phe Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu
145 150 155 160

Arg Arg Glu Ala Glu Lys Gly Lys Pro Val Thr Leu Lys Asp Ile Phe
165 170 175

Gly Ala Tyr Ser Met Asp Val Ile Thr Gly Thr Ser Phe Gly Val Asn
180 185 190

Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Ser Thr Lys
195 200 205

Lys Phe Leu Lys Phe Gly Phe Leu Asp Pro Leu Phe Leu Ser Ile Ile
210 215 220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ala Leu Asn Val Ser Leu
225 230 235 240

Phe Pro Lys Asp Thr Ile Asn Phe Leu Ser Lys Ser Val Asn Arg Met
245 250 255

Lys Lys Ser Arg Leu Asn Asp Lys Gln Lys His Arg Leu Asp Phe Leu
260 265 270

Gln Leu Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Glu Ser His Lys

20/31

275 280 285

Ala Leu Ser Asp Leu Glu Leu Ala Ala Gln Ser Ile Ile Phe Ile Phe
 290 295 300

Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Thr Leu Tyr Glu
 305 310 315 320

Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Lys Glu Ile Asp
 325 330 335

Ala Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Ala Val Val Gln
 340 345 350

Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro
 355 360 365

Val Ala Ile Arg Leu Glu Arg Thr Cys Lys Lys Asp Val Glu Ile Asn
 370 375 380

Gly Val Phe Ile Pro Lys Gly Ser Met Val Val Ile Pro Thr Tyr Ala
 385 390 395 400

Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Glu Phe Arg Pro
 405 410 415

Glu Arg Phe Ser Lys Lys Asp Ser Ile Asp Pro Tyr Ile Tyr Thr
 420 425 430

Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala Leu
 435 440 445

Met Asn Met Lys Leu Ala Leu Ile Arg Val Leu Gln Asn Phe Ser Phe
 450 455 460

Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asp Thr Gln Gly
 465 470 475 480

Leu Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val Asp Ser Arg Asp
 485 490 495

Gly Thr Leu Ser Gly Glu
 500

<210> 13

<211> 503

<212> PRT

<213> Homo sapiens

<220>

<223> CYP3A43

<400> 13

Met Asp Leu Ile Pro Asn Phe Ala Met Glu Thr Trp Val Leu Val Ala
 1 5 10 15

Thr Ser Leu Val Leu Leu Tyr Ile Tyr Gly Thr His Ser His Lys Leu
 20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly
35 40 45

Thr Ile Leu Phe Tyr Leu Arg Gly Leu Trp Asn Phe Asp Arg Glu Cys
50 55 60

Asn Glu Lys Tyr Gly Glu Met Trp Gly Leu Tyr Glu Gly Gln Gln Pro
65 70 75 80

Met Leu Val Ile Met Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
85 90 95

Glu Cys Tyr Ser Val Phe Thr Asn Gln Met Pro Leu Gly Pro Met Gly
100 105 110

Phe Leu Lys Ser Ala Leu Ser Phe Ala Glu Asp Glu Glu Trp Lys Arg
115 120 125

Ile Arg Thr Leu Leu Ser Pro Ala Phe Thr Ser Val Lys Phe Lys Glu
130 135 140

Met Val Pro Ile Ile Ser Gln Cys Gly Asp Met Leu Val Arg Ser Leu
145 150 155 160

Arg Gln Glu Ala Glu Asn Ser Lys Ser Ile Asn Leu Lys Asp Phe Phe
165 170 175

Gly Ala Tyr Thr Met Asp Val Ile Thr Gly Thr Leu Phe Gly Val Asn
180 185 190

Leu Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Leu Lys Asn Met Lys
195 200 205

Lys Leu Leu Lys Leu Asp Phe Leu Asp Pro Phe Leu Leu Ile Ser
210 215 220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ala Leu Asn Ile Gly Leu
225 230 235 240

Phe Pro Lys Asp Val Thr His Phe Leu Lys Asn Ser Ile Glu Arg Met
245 250 255

Lys Glu Ser Arg Leu Lys Asp Lys Gln Lys His Arg Val Asp Phe Phe
260 265 270

Gln Gln Met Ile Asp Ser Gln Asn Ser Lys Glu Thr Lys Ser His Lys
275 280 285

Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Ile Ile Phe
290 295 300

Ala Ala Tyr Asp Thr Thr Ser Thr Thr Leu Pro Phe Ile Met Tyr Glu
305 310 315 320

Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp
325 330 335

Ala Val Leu Pro Asn Lys Ala Pro Val Thr Tyr Asp Ala Leu Val Gln
340 345 350

Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro

355 360 365

Val Val Ser Arg Val Thr Arg Val Cys Lys Lys Asp Ile Glu Ile Asn
370 375 380

Gly Val Phe Ile Pro Lys Gly Leu Ala Val Met Val Pro Ile Tyr Ala
385 390 395 400

Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Cys Pro
405 410 415

Glu Arg Phe Ser Lys Lys Asn Lys Asp Ser Ile Asp Leu Tyr Arg Tyr
420 425 430

Ile Pro Phe Gly Ala Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
435 440 445

Leu Thr Asn Ile Lys Leu Ala Val Ile Arg Ala Leu Gln Asn Phe Ser
450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asp Asn Leu
465 470 475 480

Pro Ile Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val His Leu Arg
485 490 495

Asp Gly Ile Thr Ser Gly Pro
500

<210> 14
<211> 501
<212> PRT
<213> Rabbit

<220>
<223> CYP3A6

<400> 14

Met Asp Leu Ile Phe Ser Leu Glu Thr Trp Val Leu Leu Ala Ala Ser
1 5 10 15

Leu Val Leu Leu Tyr Leu Tyr Gly Thr Ser Thr His Gly Leu Phe Lys
20 25 30

Lys Met Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Ile Gly Thr Ile
35 40 45

Leu Glu Tyr Arg Lys Gly Ile Trp Asp Phe Asp Ile Glu Cys Arg Lys
50 55 60

Lys Tyr Gly Lys Met Trp Gly Leu Phe Asp Gly Arg Gln Pro Leu Met
65 70 75 80

Val Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys Glu Cys
85 90 95

Tyr Ser Val Phe Thr Asn Arg Arg Ser Phe Gly Pro Val Gly Phe Met
100 105 110

Lys Lys Ala Val Ser Ile Ser Glu Asp Glu Asp Trp Lys Arg Val Arg
115 120 125

Thr Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu Met Leu
130 135 140

Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Lys Asn Leu Arg Gln
145 150 155 160

Glu Ala Glu Lys Gly Lys Pro Val Asp Leu Lys Glu Ile Phe Gly Ala
165 170 175

Tyr Ser Met Asp Val Ile Thr Gly Thr Ser Phe Gly Val Asn Ile Asp
180 185 190

Ser Leu Arg Asn Pro Gln Asp Pro Phe Val Lys Asn Val Arg Arg Leu
195 200 205

Leu Lys Phe Ser Phe Phe Asp Pro Leu Leu Leu Ser Ile Thr Leu Phe
210 215 220

Pro Phe Leu Thr Pro Ile Phe Glu Ala Leu His Ile Ser Met Phe Pro
225 230 235 240

Lys Asp Val Met Asp Phe Leu Lys Thr Ser Val Glu Lys Ile Lys Asp
245 250 255

Asp Arg Leu Lys Asp Lys Gln Lys Arg Arg Val Asp Phe Leu Gln Leu
260 265 270

Met Ile Asn Ser Gln Asn Ser Lys Glu Ile Asp Ser His Lys Ala Leu
275 280 285

Asp Asp Ile Glu Val Val Ala Gln Ser Ile Ile Ile Leu Phe Ala Gly
290 295 300

Tyr Glu Thr Thr Ser Ser Thr Leu Ser Phe Ile Met His Leu Leu Ala
305 310 315 320

Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp Thr Leu
325 330 335

Leu Pro Asn Lys Glu Leu Ala Thr Tyr Asp Thr Leu Val Lys Met Glu
340 345 350

Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro Ile Ala
355 360 365

Gly Arg Leu Glu Arg Val Cys Lys Lys Asp Val Asp Ile Asn Gly Thr
370 375 380

Phe Ile Pro Lys Gly Thr Ile Val Met Met Pro Thr Tyr Ala Leu His
385 390 395 400

Arg Asp Pro Gln His Trp Thr Glu Pro Asp Glu Phe Arg Pro Glu Arg
405 410 415

Phe Ser Lys Lys Asn Lys Asp Asn Ile Asn Pro Tyr Ile Tyr His Pro
420 425 430

Phe Gly Ala Gly Pro Arg Asn Cys Leu Gly Met Arg Phe Ala Leu Met

435

440

445

Asn Ile Lys Leu Ala Leu Val Arg Leu Met Gln Asn Phe Ser Phe Lys
450 455 460

Leu Cys Lys Glu Thr Gln Val Pro Leu Lys Leu Gly Lys Gln Gly Leu
465 470 475 480

Leu Gln Pro Glu Lys Pro Ile Val Leu Lys Val Val Ser Arg Asp Gly
485 490 495

Ile Ile Arg Gly Ala
500

<210> 15

<211> 503

<212> PRT

<213> Homo sapiens

<220>

<223> CYP3A7

<400> 15

Met Asp Leu Ile Pro Asn Leu Ala Val Glu Thr Trp Leu Leu Leu Ala
1 5 10 15

Val Ser Leu Ile Leu Leu Tyr Leu Tyr Gly Thr Arg Thr His Gly Leu
20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Leu Gly
35 40 45

Asn Ala Leu Ser Phe Arg Lys Gly Tyr Trp Thr Phe Asp Met Glu Cys
50 55 60

Tyr Lys Lys Tyr Arg Lys Val Trp Gly Ile Tyr Asp Cys Gln Gln Pro
65 70 75 80

Met Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
85 90 95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Pro Phe Gly Pro Val Gly
100 105 110

Phe Met Lys Asn Ala Ile Ser Ile Ala Glu Asp Glu Glu Trp Lys Arg
115 120 125

Ile Arg Ser Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
130 135 140

Met Val Pro Ile Ile Ala Gln Tyr Gly Asp Val Leu Val Arg Asn Leu
145 150 155 160

Arg Arg Glu Ala Glu Thr Gly Lys Pro Val Thr Leu Lys His Val Phe
165 170 175

Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Ser
180 185 190

Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Thr Lys
195 200 205

Lys Leu Leu Arg Phe Asn Pro Leu Asp Pro Phe Val Leu Ser Ile Lys
210 215 220

Val Phe Pro Phe Leu Thr Pro Ile Leu Glu Ala Leu Asn Ile Thr Val
225 230 235 240

Phe Pro Arg Lys Val Ile Ser Phe Leu Thr Lys Ser Val Lys Gln Ile
245 250 255

Lys Glu Gly Arg Leu Lys Glu Thr Gln Lys His Arg Val Asp Phe Leu
260 265 270

Gln Leu Met Ile Asp Ser Gln Asn Ser Lys Asp Ser Glu Thr His Lys
275 280 285

Ala Leu Ser Asp Leu Glu Leu Met Ala Gln Ser Ile Ile Phe Ile Phe
290 295 300

Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu Ser Phe Ile Ile Tyr Glu
305 310 315 320

Leu Ala Thr His Pro Asp Val Gln Gln Lys Val Gln Lys Glu Ile Asp
325 330 335

Thr Val Leu Pro Asn Lys Ala Pro Pro Thr Tyr Asp Thr Val Leu Gln
340 345 350

Leu Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Phe Pro
355 360 365

Val Ala Met Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Asn
370 375 380

Gly Met Phe Ile Pro Lys Gly Val Val Met Ile Pro Ser Tyr Val
385 390 395 400

Leu His His Asp Pro Lys Tyr Trp Thr Glu Pro Glu Lys Phe Leu Pro
405 410 415

Glu Arg Phe Ser Lys Lys Asn Lys Asp Asn Ile Asp Pro Tyr Ile Tyr
420 425 430

Thr Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
435 440 445

Leu Val Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser
450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Arg Phe Gly
465 470 475 480

Gly Leu Leu Leu Thr Glu Lys Pro Ile Val Leu Lys Ala Glu Ser Arg
485 490 495

Asp Glu Thr Val Ser Gly Ala
500

<210> 16
<211> 503
<212> PRT
<213> Dog

<220>
<223> CYP3A12

<400> 16

Met Asp Leu Ile Pro Ser Phe Ser Thr Glu Thr Trp Leu Leu Leu Ala
1 5 10 15

Ile Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Tyr Thr His Gly Ile
20 25 30

Phe Arg Lys Leu Gly Ile Pro Gly Pro Thr Pro Leu Pro Phe Val Gly
35 40 45

Thr Ala Leu Gly Tyr Arg Asn Gly Phe Tyr Val Phe Asp Met Lys Cys
50 55 60

Phe Ser Lys Tyr Gly Arg Met Trp Gly Phe Tyr Asp Gly Arg Gln Pro
65 70 75 80

Val Leu Ala Ile Thr Asp Pro Asp Met Ile Lys Thr Val Leu Val Lys
85 90 95

Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Thr Leu Gly Pro Val Gly
100 105 110

Phe Met Lys Ser Ala Ile Ser Leu Ser Glu Asp Glu Glu Trp Lys Arg
115 120 125

Met Arg Thr Leu Leu Ser Pro Thr Phe Thr Thr Gly Lys Leu Lys Glu
130 135 140

Met Phe Pro Ile Ile Gly Gln Tyr Gly Asp Val Leu Val Asn Asn Leu
145 150 155 160

Arg Lys Glu Ala Glu Lys Gly Lys Ala Ile Asn Leu Lys Asp Val Phe
165 170 175

Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ser Phe Gly Val Asn
180 185 190

Ile Asp Ser Leu Asn His Pro Gln Asp Pro Phe Val Glu Asn Thr Lys
195 200 205

Lys Leu Leu Lys Phe Asp Phe Leu Asp Pro Phe Phe Ser Ile Leu
210 215 220

Leu Phe Pro Phe Leu Thr Pro Val Phe Glu Ile Leu Asn Ile Trp Leu
225 230 235 240

Phe Pro Lys Lys Val Thr Asp Phe Phe Arg Lys Ser Val Glu Arg Met
245 250 255

Lys Glu Ser Arg Leu Lys Asp Lys Gln Lys His Arg Val Asp Phe Leu
260 265 270

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Gln Leu Met Ile Asn Ser Gln Asn Ser Lys Glu Met Asp Thr His Lys
275 280 285

Ala Leu Ser Asp Leu Glu Leu Val Ala Gln Ser Ile Ile Phe Ile Phe
290 295 300

Ala Gly Tyr Glu Thr Thr Ser Thr Ser Leu Ser Phe Leu Met Tyr Glu
305 310 315 320

Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Asp
325 330 335

Ala Thr Phe Pro Asn Lys Ala Leu Pro Thr Tyr Asp Ala Leu Val Gln
340 345 350

Met Glu Tyr Leu Asp Met Val Leu Asn Glu Thr Leu Arg Leu Tyr Pro
355 360 365

Ile Ala Gly Arg Leu Glu Arg Val Cys Lys Lys Asp Val Glu Ile Ser
370 375 380

Gly Val Phe Ile Pro Lys Gly Thr Val Val Met Val Pro Thr Phe Thr
385 390 395 400

Leu His Arg Asp Gln Ser Leu Trp Pro Glu Pro Glu Glu Phe Arg Pro
405 410 415

Glu Arg Phe Ser Arg Lys Asn Lys Asp Ser Ile Asn Pro Tyr Thr Tyr
420 425 430

Leu Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
435 440 445

Ile Met Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser
450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Asn Ala Gln
465 470 475 480

Gly Ile Ile Gln Pro Glu Lys Pro Ile Val Leu Lys Val Glu Pro Arg
485 490 495

Asp Gly Ser Val Asn Gly Ala
500

<210> 17
<211> 503
<212> PRT
<213> Pig

<220>
<223> CYP3A29

<400> 17

Met Asp Leu Ile Pro Gly Phe Ser Thr Glu Thr Trp Val Leu Leu Ala
1 5 10 15

Thr Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr Tyr Ser His Gly Leu
20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Arg Pro Leu Pro Tyr Phe Gly
 35 40 45
 Asn Ile Leu Gly Tyr Arg Lys Gly Val Asp His Phe Asp Lys Lys Cys
 50 55 60
 Phe Gln Gln Tyr Gly Lys Met Trp Gly Val Tyr Asp Gly Arg Gln Pro
 65 70 75 80
 Leu Leu Ala Val Thr Asp Pro Asn Met Ile Lys Ser Val Leu Val Lys
 85 90 95
 Glu Cys Tyr Ser Val Phe Thr Asn Arg Arg Ser Phe Gly Pro Leu Gly
 100 105 110
 Ala Met Arg Asn Ala Leu Ser Leu Ala Glu Asp Glu Glu Trp Lys Arg
 115 120 125
 Ile Arg Thr Leu Leu Ser Pro Thr Phe Thr Ser Gly Lys Leu Lys Glu
 130 135 140
 Met Phe Pro Ile Ile Ser His Tyr Gly Asp Leu Leu Val Ser Asn Leu
 145 150 155 160
 Arg Lys Glu Ala Glu Lys Gly Lys Pro Val Thr Met Lys Asp Ile Phe
 165 170 175
 Gly Ala Tyr Ser Met Asp Val Ile Thr Ser Thr Ala Phe Gly Val Asn
 180 185 190
 Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Asn Ser Lys
 195 200 205
 Lys Leu Leu Lys Phe Ser Phe Phe Asp Pro Phe Leu Leu Ser Leu Ile
 210 215 220
 Phe Phe Pro Phe Leu Thr Pro Ile Phe Glu Val Leu Asn Ile Thr Leu
 225 230 235 240
 Phe Pro Lys Ser Ser Val Asn Phe Phe Thr Lys Ser Val Lys Arg Met
 245 250 255
 Lys Glu Ser Arg Leu Thr Asp Gln Gln Lys Arg Arg Val Asp Leu Leu
 260 265 270
 Gln Leu Met Ile Asn Ser Gln Asn Ser Lys Glu Met Asp Pro His Lys
 275 280 285
 Ser Leu Ser Asn Glu Glu Leu Val Ala Gln Gly Ile Ile Phe Ile Phe
 290 295 300
 Ala Gly Tyr Glu Thr Thr Ser Ser Ala Leu Ser Leu Leu Ala Tyr Glu
 305 310 315 320
 Leu Ala Thr His Pro Asp Val Gln Gln Lys Leu Gln Glu Glu Ile Glu
 325 330 335
 Ala Thr Phe Pro Asn Lys Ala Pro Pro Thr Tyr Asp Ala Leu Ala Gln
 340 345 350

Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro
355 360 365

Ile Ala Ala Arg Leu Glu Arg Ala Cys Lys Lys Asp Val Glu Ile His
370 375 380

Gly Val Phe Val Pro Lys Gly Thr Val Val Val Val Pro Val Phe Val
385 390 395 400

Leu His Arg Asp Pro Asp Leu Trp Pro Glu Pro Glu Glu Phe Arg Pro
405 410 415

Glu Arg Phe Ser Lys His Lys Asp Thr Ile Asn Pro Tyr Thr Tyr
420 425 430

Leu Pro Phe Gly Thr Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
435 440 445

Leu Met Asn Met Lys Leu Ala Leu Val Arg Val Leu Gln Asn Phe Ser
450 455 460

Phe Lys Pro Cys Lys Glu Thr Gln Ile Pro Leu Lys Leu Thr Thr Gln
465 470 475 480

Gly Leu Thr Gln Pro Glu Lys Pro Val Val Leu Lys Ile Leu Pro Arg
485 490 495

Asp Gly Thr Val Ser Gly Ala
500

<210> 18

<211> 503

<212> PRT

<213> Mouse

<220>

<223> CYP3A13

<400> 18

Met Asp Leu Ile Pro Asn Phe Ser Met Glu Thr Trp Met Leu Leu Ala
1 5 10 15

Thr Ser Leu Val Leu Leu Tyr Leu Tyr Gly Thr His Ser His Gly Ile
20 25 30

Phe Lys Lys Leu Gly Ile Pro Gly Pro Lys Pro Leu Pro Phe Leu Gly
35 40 45

Thr Ile Leu Ala Tyr Gln Lys Gly Phe Trp Glu Cys Asp Ile Gln Cys
50 55 60

His Lys Lys Tyr Gly Lys Met Trp Gly Leu Tyr Asp Gly Arg Gln Pro
65 70 75 80

Val Leu Ala Ile Thr Asp Pro Asp Ile Ile Lys Thr Val Leu Val Lys
85 90 95

Glu Cys Tyr Ser Thr Phe Thr Asn Arg Arg Arg Phe Gly Pro Val Gly
100 105 110
Ile Leu Lys Lys Ala Ile Ser Ile Ser Glu Asn Glu Glu Trp Lys Arg
115 120 125
Ile Arg Ala Leu Leu Ser Pro Thr Phe Thr Ser Gly Arg Leu Lys Glu
130 135 140
Met Phe Pro Ile Ile Asn Gln Phe Thr Asp Val Leu Val Arg Asn Met
145 150 155 160
Arg Gln Gly Leu Gly Glu Gly Lys Pro Thr Ser Met Lys Asp Ile Phe
165 170 175
Gly Ala Tyr Ser Met Asp Val Ile Thr Ala Thr Ser Phe Gly Val Asn
180 185 190
Ile Asp Ser Leu Asn Asn Pro Gln Asp Pro Phe Val Glu Lys Ile Lys
195 200 205
Lys Leu Leu Lys Phe Asp Ile Phe Asp Pro Leu Phe Leu Ser Val Thr
210 215 220
Leu Phe Pro Phe Leu Thr Pro Val Phe Asp Ala Leu Asn Val Ser Leu
225 230 235 240
Phe Pro Arg Asp Val Ile Ser Phe Phe Thr Thr Ser Val Glu Arg Met
245 250 255
Lys Glu Asn Arg Met Lys Glu Lys Glu Lys Gln Arg Val Asp Phe Leu
260 265 270
Gln Leu Met Ile Asn Ser Gln Asn Tyr Lys Thr Lys Glu Ser His Lys
275 280 285
Ala Leu Ser Asp Val Glu Ile Val Ala Gln Ser Val Ile Phe Ile Phe
290 295 300
Ala Gly Tyr Glu Thr Thr Ser Ser Ala Leu Ser Phe Ala Leu Tyr Leu
305 310 315 320
Leu Ala Ile His Pro Asp Val Gln Lys Lys Leu Gln Asp Glu Ile Asp
325 330 335
Ala Ala Leu Pro Asn Lys Ala Pro Ala Thr Tyr Asp Thr Leu Leu Gln
340 345 350
Met Glu Tyr Leu Asp Met Val Val Asn Glu Thr Leu Arg Leu Tyr Pro
355 360 365
Ile Ala Gly Arg Leu Glu Arg Val Cys Lys Thr Asp Val Glu Ile Asn
370 375 380
Gly Leu Phe Ile Pro Lys Gly Thr Val Val Met Ile Pro Thr Phe Ala
385 390 395 400
Leu His Lys Asp Pro Lys Tyr Trp Pro Glu Pro Glu Glu Phe Arg Pro
405 410 415

Glu Arg Phe Ser Lys Lys Asn Gln Asp Ser Ile Asn Pro Tyr Met Tyr
420 425 430

Leu Pro Phe Gly Ser Gly Pro Arg Asn Cys Ile Gly Met Arg Phe Ala
435 440 445

Leu Ile Asn Met Lys Val Ala Leu Val Arg Val Leu Gln Asn Phe Thr
450 455 460

Val Gln Pro Cys Lys Glu Thr Glu Ile Pro Leu Lys Leu Ser Lys Gln
465 470 475 480

Gly Leu Leu Gln Pro Glu Asn Pro Leu Leu Leu Lys Val Val Ser Arg
485 490 495

Asp Glu Thr Val Ser Asp Glu
500